



SEQUENCE LISTING

<110> PEDERSEN, ANDERS H.
ANDERSON, KIM V.
BORNAES, CLAUS

<120> FACTOR VII OR VIIA-LIKE MOLECULES

<130> 31-001100US

<140> 09/782,587

<141> 2001-02-12

<150> PA 2000 00218

<151> 2000-02-11

<150> 60/184,036

<151> 2000-02-22

<150> 60/241,916

<151> 2000-10-18

<160> 19

<170> PatentIn Ver. 2.1

<210> 1

<211> 406

<212> PRT

<213> Homo sapiens

<220>

<221> MOD_RES

<222> (6)..(7)

<223> Gamma carboxyglutamic acid or glutamic acid

<220>

<221> MOD_RES

<222> (14)

<223> Gamma carboxyglutamic acid or glutamic acid

<220>

<221> MOD_RES

<222> (16)

<223> Gamma carboxyglutamic acid or glutamic acid

<220>

<221> MOD_RES

<222> (19)..(20)

<223> Gamma carboxyglutamic acid or glutamic acid

<220>

<221> MOD_RES

<222> (25)..(26)

<223> Gamma carboxyglutamic acid or glutamic acid

<220>

<221> MOD_RES

#7

<222> (29)

<223> Gamma carboxyglutamic acid or glutamic acid

<220>

<221> MOD_RES

<222> (35)

<223> Gamma carboxyglutamic acid or glutamic acid

<400> 1

Ala Asn Ala Phe Leu Xaa Xaa Leu Arg Pro Gly Ser Leu Xaa Arg Xaa
1 5 10 15

Cys Lys Xaa Xaa Gln Cys Ser Phe Xaa Xaa Ala Arg Xaa Ile Phe Lys
20 25 30

Asp Ala Xaa Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp
35 40 45

Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln
50 55 60

Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn
65 70 75 80

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
85 90 95

Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
100 105 110

Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
115 120 125

Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
130 135 140

Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
145 150 155 160

Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
165 170 175

Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
180 185 190

His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
195 200 205

Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
210 215 220

Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
225 230 235 240

His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
245 250 255

His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
 260 265 270
 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
 275 280 285
 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
 290 295 300
 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
 305 310 315 320
 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
 325 330 335
 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
 340 345 350
 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
 355 360 365
 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
 370 375 380
 Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
 385 390 395 400
 Leu Arg Ala Pro Phe Pro
 405

<210> 2
 <211> 1338
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (115)..(1332)

<400> 2
 atggtcagcc aggccctccg cctcctgtgc ctgctcctgg ggctgcaggg ctgcctggct 60
 gccgtcttcg tcacccagga ggaagcccat ggcgtcctgc atcgccggcg ccgg gcc 117
 Ala
 1
 aat gcc ttt ctg gaa gag ctc cgc cct ggc tcc ctg gaa cgc gaa tgc 165
 Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
 5 10 15
 aaa gag gaa cag tgc agc ttt gag gaa gcc cgg gag att ttc aaa gac 213
 Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp
 20 25 30
 gct gag cgg acc aaa ctg ttt tgg att agc tat agc gat ggc gat cag 261
 Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln
 35 40 45

tgc gcc tcc agc cct tgc cag aac ggg ggc tcc tgc aaa gac cag ctg	309
Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu	
50 55 60 65	
cag agc tat atc tgc ttc tgc ctg cct gcc ttt gag ggg cgc aat tgc	357
Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn Cys	
70 75 80	
gaa acc cat aag gat gac cag ctg att tgc gtc aac gaa aac ggg ggc	405
Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly Gly	
85 90 95	
tgc gag cag tac tgc agc gat cac acg ggc acg aag cgg agc tgc cgc	453
Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys Arg	
100 105 110	
tgc cac gaa ggc tat agc ctc ctg gct gac ggg gtg tcc tgc acg ccc	501
Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro	
115 120 125	
acg gtg gaa tac cct tgc ggg aag att ccc att cta gaa aag cgg aac	549
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn	
130 135 140 145	
gct agc aaa ccc cag ggc cgg atc gtc ggc ggg aag gtc tgc cct aag	597
Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys	
150 155 160	
ggg gag tgc ccc tgg cag gtc ctg ctc ctg gtc aac ggg gcc cag ctg	645
Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln Leu	
165 170 175	
tgc ggc ggg acc ctc atc aat acc att tgg gtc gtg tcc gcc gct cac	693
Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala His	
180 185 190	
tgc ttc gat aag att aag aat tgg cgg aac ctc atc gct gtg ctc ggc	741
Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu Gly	
195 200 205	
gaa cac gat ctg tcc gag cat gac ggg gac gaa cag tcc cgc cgg gtg	789
Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg Val	
210 215 220 225	
gct cag gtc atc att ccc tcc acc tat gtg cct ggc acg acc aat cac	837
Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His	
230 235 240	
gat atc gct ctg ctc cgc ctc cac cag ccc gtc gtg ctc acc gat cac	885
Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His	
245 250 255	
gtc gtg cct ctg tgc ctg cct gag cgg acc ttt agc gaa cgc acg ctg	933
Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu	
260 265 270	

gct ttc gtc cgc ttt agc ctc gtg tcc ggc tgg ggc cag ctg ctc gac	981
Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu Asp	
275 280 285	
cgg ggc gct acc gct ctc gag ctg atg gtg ctc aac gtc ccc cgg ctg	1029
Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg Leu	
290 295 300 305	
atg acc cag gac tgc ctg cag cag tcc cgc aaa gtg ggg gac tcc ccc	1077
Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser Pro	
310 315 320	
aat atc acg gag tat atg ttt tgc gct ggc tat agc gat ggc tcc aag	1125
Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser Lys	
325 330 335	
gat agc tgc aag ggg gac tcc ggc ggg ccc cat gcc acg cac tat cgc	1173
Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg	
340 345 350	
ggg acc tgg tac ctc acc ggg atc gtc agc tgg ggc cag ggc tgc gcc	1221
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala	
355 360 365	
acg gtg ggg cac ttt ggc gtc tac acg cgc gtc agc cag tac att gag	1269
Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu	
370 375 380 385	
tgg ctg cag aag ctc atg cgg agc gaa ccc cgg ccc ggg gtg ctc ctg	1317
Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu Leu	
390 395 400	
cgg gcc cct ttc cct tgataa	1338
Arg Ala Pro Phe Pro	
405	

<210> 3
 <211> 406
 <212> PRT
 <213> Homo sapiens

<400> 3	
Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu	
1 5 10 15	
Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys	
20 25 30	
Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp	
35 40 45	
Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly Gly Ser Cys Lys Asp Gln	
50 55 60	
Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro Ala Phe Glu Gly Arg Asn	
65 70 75 80	

Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val Asn Glu Asn Gly
 85 90 95
 Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg Ser Cys
 100 105 110
 Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr
 115 120 125
 Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg
 130 135 140
 Asn Ala Ser Lys Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro
 145 150 155 160
 Lys Gly Glu Cys Pro Trp Gln Val Leu Leu Leu Val Asn Gly Ala Gln
 165 170 175
 Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile Trp Val Val Ser Ala Ala
 180 185 190
 His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile Ala Val Leu
 195 200 205
 Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg Arg
 210 215 220
 Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn
 225 230 235 240
 His Asp Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp
 245 250 255
 His Val Val Pro Leu Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr
 260 265 270
 Leu Ala Phe Val Arg Phe Ser Leu Val Ser Gly Trp Gly Gln Leu Leu
 275 280 285
 Asp Arg Gly Ala Thr Ala Leu Glu Leu Met Val Leu Asn Val Pro Arg
 290 295 300
 Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg Lys Val Gly Asp Ser
 305 310 315 320
 Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp Gly Ser
 325 330 335
 Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr
 340 345 350
 Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys
 355 360 365
 Ala Thr Val Gly His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile
 370 375 380

Glu Trp Leu Gln Lys Leu Met Arg Ser Glu Pro Arg Pro Gly Val Leu
 385 390 395 400

Leu Arg Ala Pro Phe Pro
 405

<210> 4
 <211> 1357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Expression
 cassette for expression of FVII in mammalian cells

<400> 4
 ggatcccgcc accatgggtca gccaggccct ccgcctcctg tgccctgctcc tggggctgca 60
 gggctgctg gctgcccgtct tcgtcaccca ggaggaagcc catggcgctcc tgcacgcgcg 120
 gegecgggcc aatgcctttc tggaagagct ccgccctggc tccctggaac gcgaatgcaa 180
 agaggaacag tgcagctttg aggaagcccg ggagattttc aaagacgctg agcggaccaa 240
 actgttttgg attagctata gcgatggcga tcagtgcgcc tccagccctt gccagaacgg 300
 gggctcctgc aaagaccagc tgcagagcta tatctgcttc tgccctgctg cctttgaggg 360
 gcgcaattgc gaaacccata aggatgacca gctgatttgc gtcaacgaaa acgggggctg 420
 cgagcagtac tgcagcgatc acacgggcac gaagcggagc tgccgctgcc acgaaggcta 480
 tagcctcctg gctgacgggg tgcctgcac gccacgggtg gaataccctt gcgggaagat 540
 tcccattcta gaaaagcgga acgctagcaa accccagggc cggatcgctc gcgggaaggt 600
 ctgccctaag ggggagtgcc cctggcaggt cctgctcctg gtcaacgggg cccagctgtg 660
 cggcgggacc ctcacataa ccatctgggt cgtgtccgcc gctcactgct tcgataagat 720
 taagaattgg cggaaacctca tcgctgtgct cggcgaacac gatctgtccg agcatgacgg 780
 ggacgaacag tcccgccggg tggctcaggt catcattccc tccacctatg tgccctggc 840
 gaccaatcac gatatcgctc tgcctcgctt ccaccagccc gtcgtgctca ccgatcacgt 900
 cgtgcctctg tgccctgctg agcggacctt tagcgaacgc acgctggctt tcgtccgctt 960
 tagcctcgtg tccggctggg gccagctgct cgaccggggc gctaccgctc tcgagctgat 1020
 ggtgctcaac gtcccccgcc tgatgaccca ggactgctg cagcagtcctt gcaaagtggg 1080
 ggactcccc aatatcacgg agtatatgtt ttgcgtggc tatagcgatg gctccaagga 1140
 tagctgcaag ggggactccg gcgggcccc tgccacgcac tatcgcgga cctgggtacct 1200
 caccgggatc gtcagctggg gccagggtg cggcacgggt gggcactttg gcgtctacac 1260
 gcgcgtcagc cagtacattg agtggtgca gaagctcatg cggagcgaac cccggcccgg 1320
 ggtgctcctg cgggcccctt tcccttgata aaagctt 1357

<210> 5
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer
 CBProFpr174

<400> 5
 agctggctag ccaactgggca ggtaagtata a

31

<210> 6
 <211> 31
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
CBProFpr175

<400> 6

tggcgggatac cttaagagct gtaattgaac t

31

<210> 7

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
CBProFpr216

<400> 7

cttaaggatac ccgccaccat ggtagccag

30

<210> 8

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
CBProFpr229

<400> 8

ggagtagcccg gttttgttgg actgctgc

28

<210> 9

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
CBProFpr221

<400> 9

acttaagctt ttatcaagg a

21

<210> 10

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer
CBProFpr228

<400> 10
gcagcagtcc aacaaaaccg gggactcc

28

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer
CBProFpr226

<400> 11
cattctagaa aaccggaccg ctagcaaacc

30

<210> 12
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide tag

<400> 12
His His His His His His
1 5

<210> 13
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide tag

<400> 13
Met Lys His His His His His His
1 5

<210> 14
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide tag

<400> 14
Met Lys His His Ala His His Gln His His
1 5 10

<210> 15
<211> 14

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide tag

<400> 15
Met Lys His Gln His Gln His Gln His Gln His Gln
1 5 10

<210> 16
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide tag

<400> 16
Met Lys His Gln His Gln His Gln His Gln His Gln His Gln
1 5 10 15

<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide tag

<400> 17
Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 18
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide tag

<400> 18
Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 19
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: synthetic peptide tag

<400> 19

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala

1

5